

From Genotype to Phenotype

Reconstructing the past:
The First Ancient Human Genome

Course:
IT and Health



Outline

- The first ancient genome
- Functional SNP assessment
- The ancient genome database
- Genome-wide association studies
- Exercise: From genotype to phenotype

First Ancient Human Genome

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The Saqqaq Genome Project

4,000 years

Hair sample from permafrost

DNA extraction <10% contamination

20 x coverage

Started 2009



The Neandertal Genome Project

38,000 years

Leg bone from a cave in Croatia

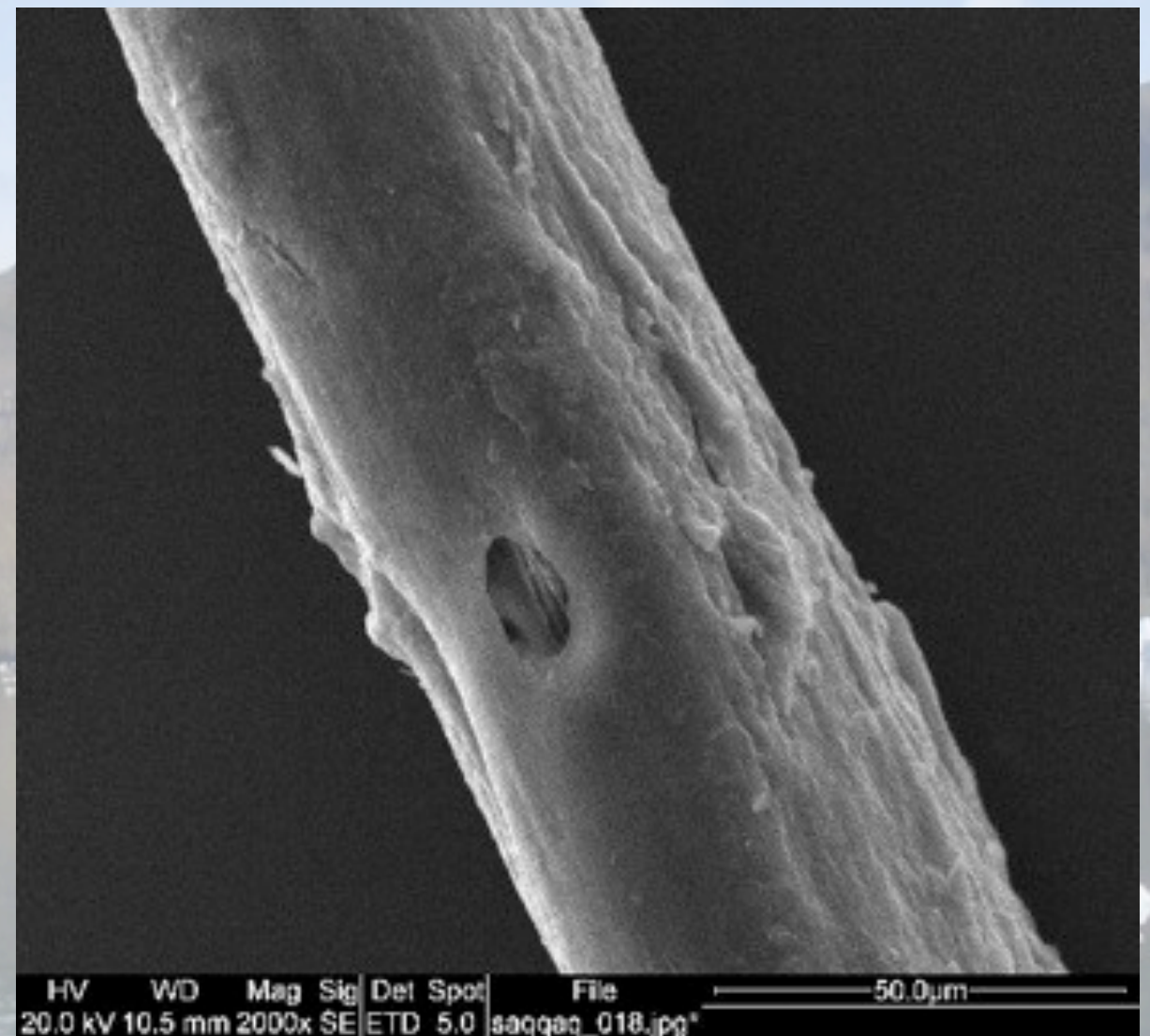
DNA extraction >95% contamination

1 x coverage

Started 2006



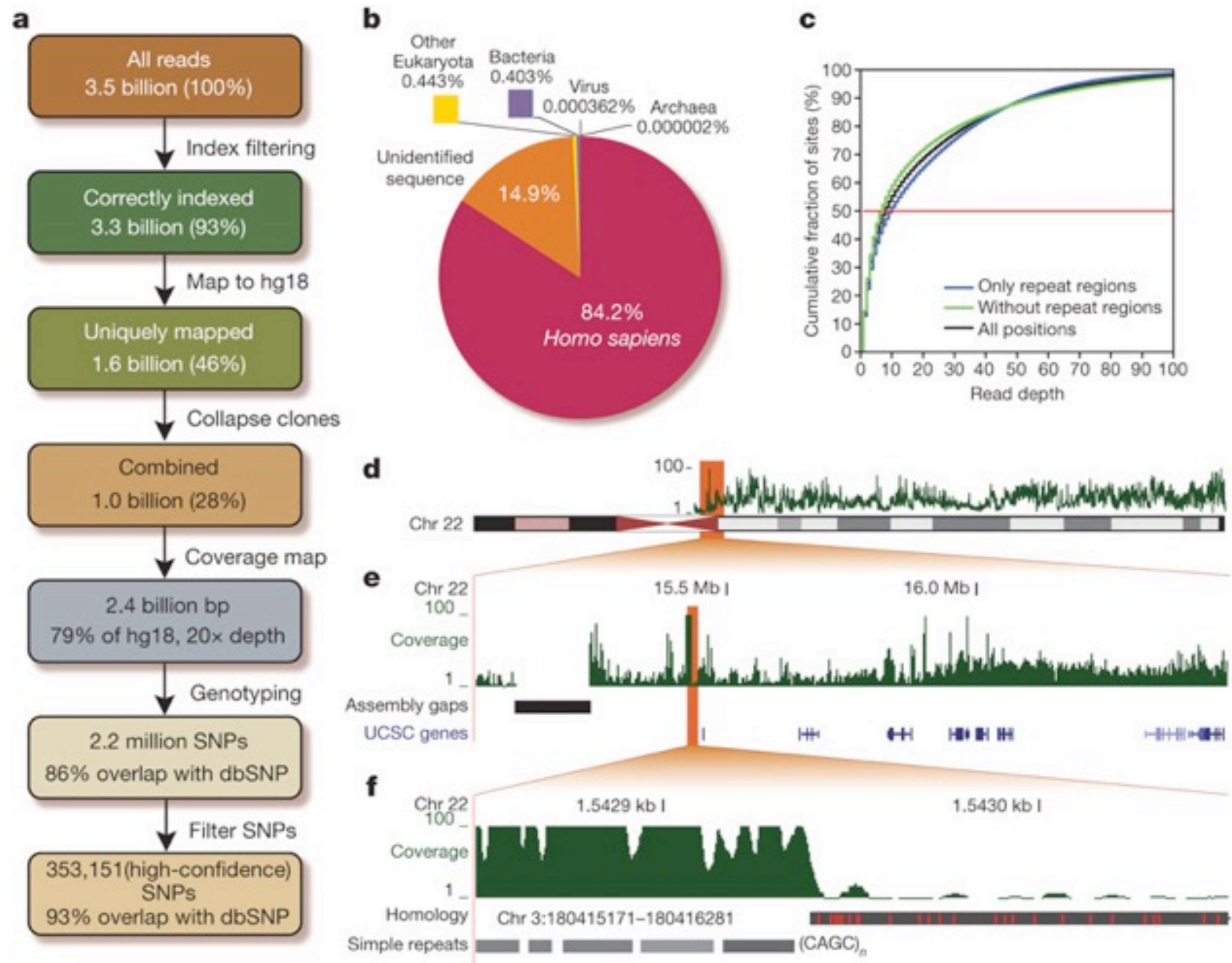
DNA from hair



DNA from hair

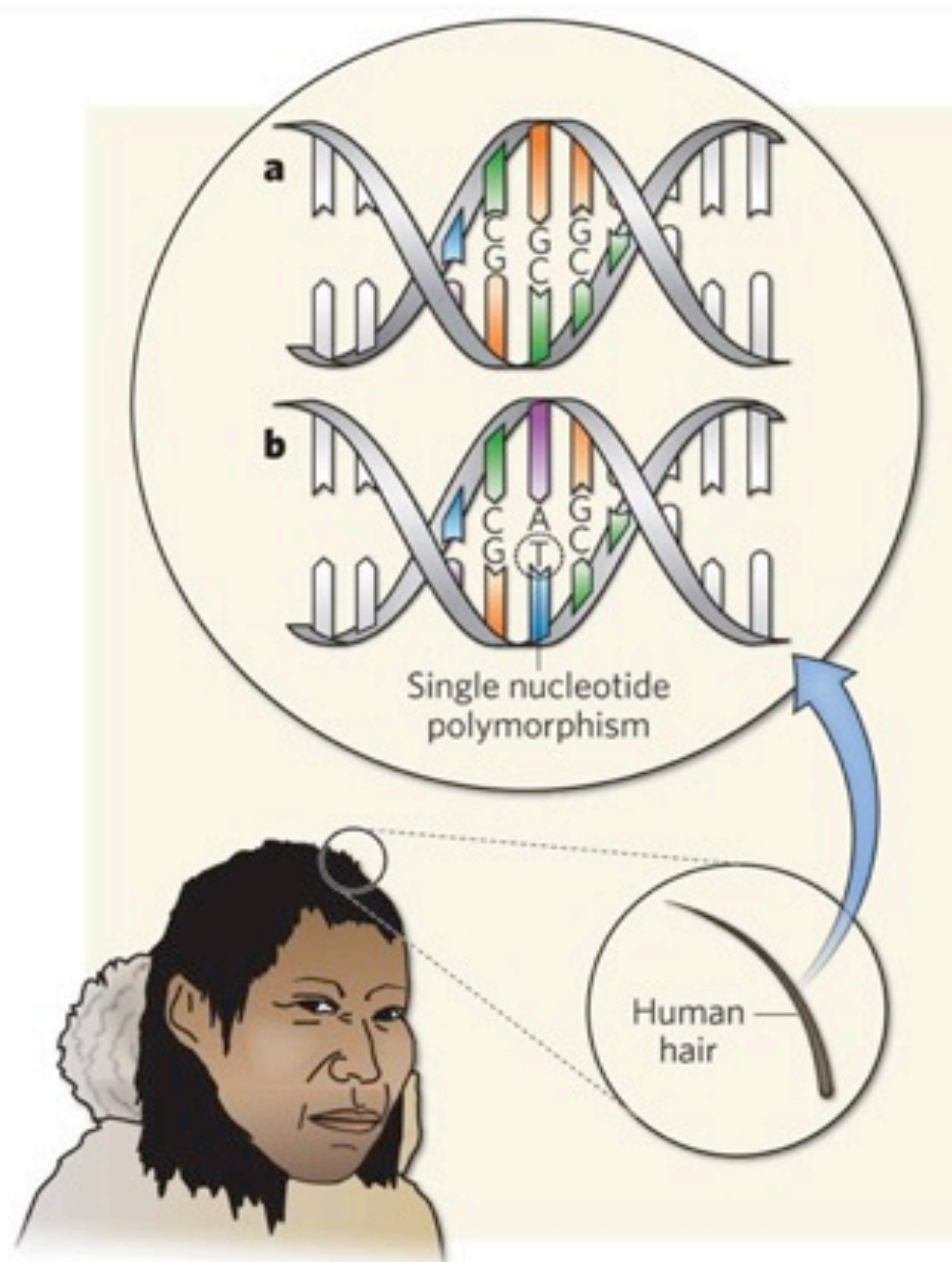
- Hardly any contamination
- Relatively high yield
- Short fragments
- <3 month sequencing
- Post-mortem DNA damage
- Polymerase Phusion

Flow chart over pipeline and data summary



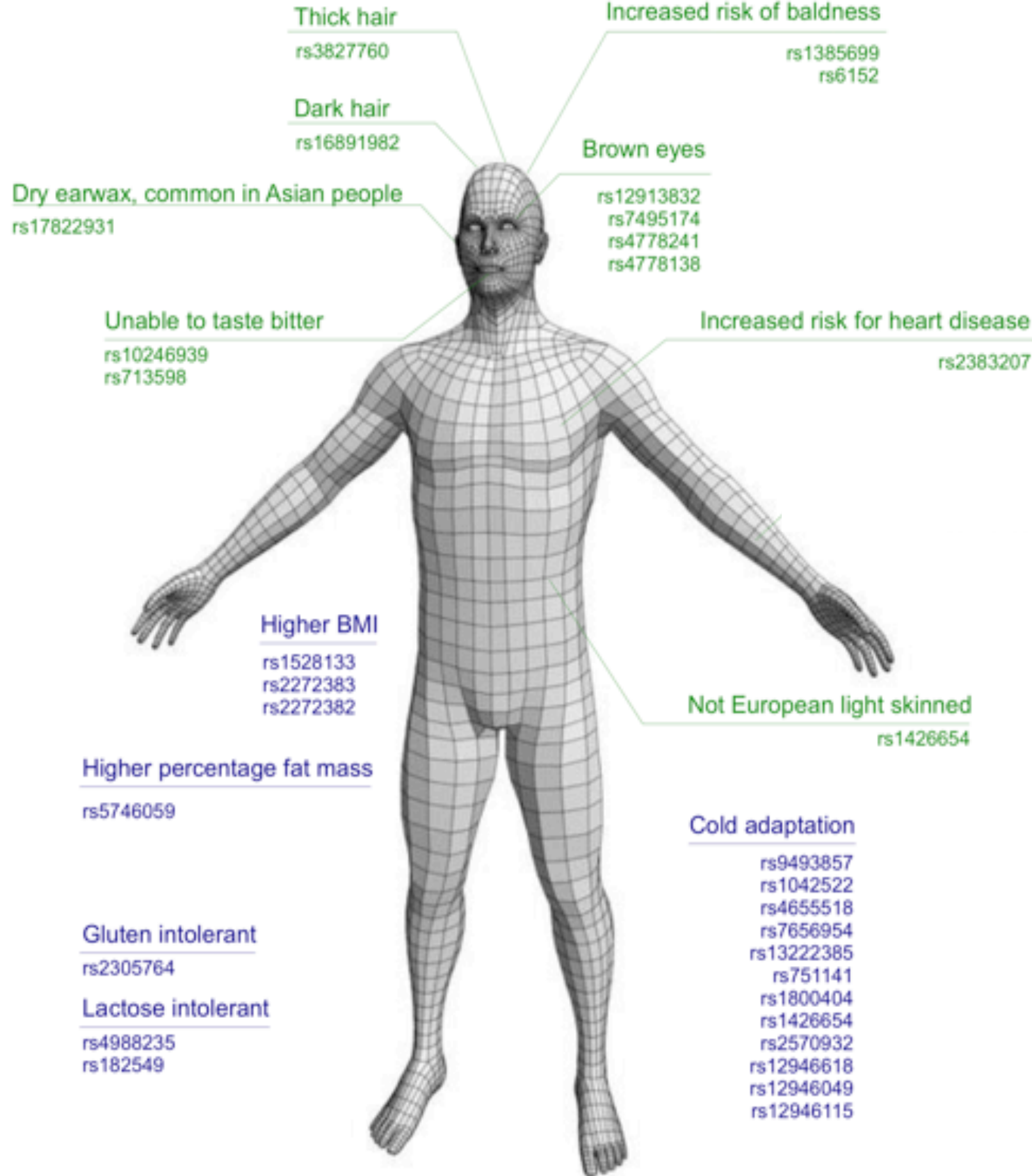
Functional SNP assessment

What can we say about his phenotype?











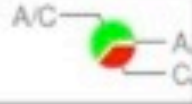



























Rasmussen *et al.*² have sequenced the genome of a man from the Saqqaq culture, using DNA from hair preserved in permafrost in Greenland. They analysed the genome to find single nucleotide polymorphisms (SNPs) — differences in single DNA base pairs that exist between individual genomes, and that may act as markers of an individual's physical traits. **a**, Here, a short stretch of human DNA is shown that is a marker for normal earwax. **b**, In the analogous DNA from the Saqqaq individual, there is a SNP in which a C in the lower strand has been replaced by a T (C, G, T and A denote the four kinds of DNA base). This SNP shows that the Saqqaq man had dry earwax. Rasmussen and colleagues identified other SNPs indicating that the ancient human had, among other things, brown eyes, non-white skin, thick dark hair and an increased susceptibility to baldness.





From genotype to phenotype: how good are we at putting a face to an anonymous individual? - While some traits manifest themselves in a tissue specific manner (highlighted in green), others are more systemic (highlighted in blue). Going from the genetic blueprint to visual appearance, physiological behaviour and medical predispositions is still an open challenge.

Table S14. List of SNP identifiers used for functional assessment. Associations to phenotype were curated from literature, public databases and HGMD Professional. Frequencies from Hapmap Phase-II are represented in pie charts, with the colour of the Saqqaq Allele matching the corresponding genotype in the pie charts. In most cases, the Saqqaq allele is closest to the Asian (Han Chinese and Japanese) populations.

SNP	Reference	1-pp	Saqqaq Allele	HapMap frequencies			
				CEU	HCB	JPT	YRI
rs8176719 ¹	66	NA	-/-	NA	NA	NA	NA
rs8176750 ²	67	8.84E-34	G/G	NA	NA	NA	NA
rs12913832 ³	68	5.13E-10	A/A				
rs7495174 ³	68	1.14E-25	A/G				
rs4778241 ³	68	8.24E-06	A/A				
rs1129038 ³	68	8.69E-40	C/C	NA	NA	NA	NA
rs1426654 ⁴	69	8.78E-12	G/G				
rs1385699 ⁵	70	8.57E-05	T/T				
rs6152 ⁵	71	4.12E-21	G/G	NA	NA	NA	NA
rs1528133 ⁶	63	1.50E-08	A/C				
rs2272383 ⁶	63	1.42E-27	A/G				
rs2272382 ⁶	63	8.40E-60	A/G				
rs5746059 ⁷	62	1.64E-05	A/A				

rs17822931 ⁸	72	8.36E-09	T/T				
rs3827760 ⁹	73	5.61E-12	C/C				
rs16891982 ¹⁰	74	3.87E-13	C/C				
rs1042522 ¹¹	75	2.75E-11	G/G				
rs13222385 ¹²	59	3.21E-05	A/G				
rs751141 ¹²	59	2.13E-07	T/T				
rs1800404 ¹²	59	2.51E-14	A/A				
rs1426654 ¹²	59	8.78E-12	G/G				
rs2570932 ¹²	59	0.001509 7	C/C				
rs12946618 ¹²	59	0.001380 2	A/A				
rs12946115 ¹²	59	2.44E-06	C/C				

¹Blood Group: not type O. ²Blood Group: A1 subtype. ³Brown eyes. ⁴Not European light skinned. ⁵Increased risk of baldness. ⁶Higher body mass index. ⁷Higher percentage fat mass in Caucasian and Chinese samples. ⁸Dry earwax, common in Asian people. ⁹Thick hair and Shovel shaped upper front teeth. ¹⁰More likely to have black hair (in European cohort study). ¹¹Cold adaptation: non-synonymous change in TP53. ¹²Cold adaptation: Metabolic genes.

The ancient genome database

www.ancientgenome.dk

- Get sequence
- Compare to reference genome (NCBI 36)
- SNP accessions
- Phenotypic associations

The Saqqaq Genome Database (beta)

Enter sequence range, identifier or cheat code

Examples

Range:	17:398382..399882 (chromosome:start..end)
SNP ID:	rs17822931 or ENSSNP22423 - Ambiguously mapped SNPs and in-deis may return several records.
List phenotypic associations on chromosome:	1:phenotype

Note: Query is currently limited to 100000 records/nucleotides

The Saqqaq Genome Database (beta)

Choose alternative output format:

Result

chr	pos	ref	is_ref	genotype	pp	depth	repeat	rs	type	strand	snp_alleles
16	46815689	C	y	CC	1.6396e-13	33					
16	46815690	T	y	TT	9.9824e-14	33					
16	46815691	T	y	TT	9.995e-14	33					
16	46815692	A	y	AA	1.01e-13	33					
16	46815693	C	y	CC	3.2608e-13	32					
16	46815694	T	y	TT	1.9992e-13	32					
16	46815695	G	y	GG	6.565e-13	31					
16	46815696	G	y	GG	6.9136e-13	31					
16	46815697	C	y	CC	1.3222e-12	30					
16	46815698	C	y	CC	2.6699e-12	29					
16	46815699	C	n	TT	8.3635e-09	28		rs17822931	single	+	CT
16	46815700	G	y	GG	1.3271e-12	30					
16	46815701	A	y	AA	2.5557e-13	31					
16	46815702	G	y	GG	2.0907e-13	32					
16	46815703	T	y	TT	6.4711e-14	33					
16	46815704	A	y	AA	1.3049e-13	32					
16	46815705	C	y	CC	4.214e-13	31					
16	46815706	A	y	AA	2.5604e-13	31					
16	46815707	C	y	CC	4.4147e-13	31					
16	46815708	T	y	TT	2.5521e-13	31					
16	46815709	G	y	GG	2.1138e-13	32					

Columns explained

chr	The chromosome
pos	Position on chromosome
ref	The reference nucleotide on leading strand in hg18
is_ref	Indicates whether the genotype is the same as the reference nucleotide (y) or not (n)
genotype	The genotype called (on leading strand)
pp	For numerical reasons, we report (1-PP), where PP is the posterior probability of the genotype
depth	The number of reads covering the position
repeat	If the position lies in an annotated repeat, the ID is given here
rs	dbSNP rs-number
type	Type of dbSNP entry ("single", "indel" etc. - see the UCSC genome browser for details).
strand	Strand for dbSNP entry + (or 1) or - (or -1)
snp_alleles	Known SNP alleles, e.g. "AC" (or "A/G") for a SNP of type "single"

Genome-wide associations studies

Cases vs controls

- Obtain DNA from a disease group (e.g. asthma) and a control group
- For each individual: Run DNA on a SNP array measuring the genotypes at almost 1M loci
- If the group consists of 1,000 individuals, one obtains 1,000 x 1,000,000 genotypes
- Quality Control
- Loop over all SNPs, and identify those that are significantly more common among cases than controls
- Those SNPs are associated with the disease
- Not necessarily causal

Example of GWAS results (asthma)

Manhattan plot displays all SNPs on x-axis (order by genomic location), and $-\log_{10}$ of p-values on y-axis.

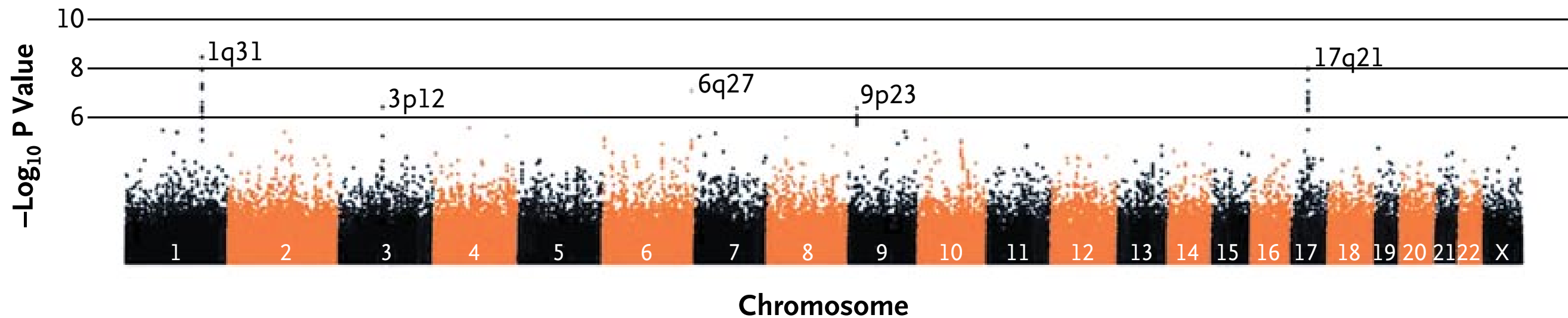


Figure 2. Manhattan Plot of the Results from the Combined Subjects of European Ancestry Who Had Asthma.

The $-\log_{10}$ P values are plotted against the physical distance. Only the two loci at chromosome 1q31 and 17q21 were significantly associated with asthma after Bonferroni correction. Individual chromosome labels are indicated in white within the Manhattan plot.

Variants of *DENND1B* Associated with Asthma in Children

Patrick M.A. Sleiman, Ph.D., James Flory, Ph.D., Marcin Imielinski, M.D., Ph.D., Jonathan P. Bradfield, B.S., Kiran Annaiah, M.Sc., Saffron A.G. Willis-Owen, Ph.D., Kai Wang, Ph.D., Nicholas M. Rafaels, M.S., Sven Michel, Ph.D., Klaus Bonnelykke, M.D., Ph.D., Haitao Zhang, Ph.D., Cecilia E. Kim, B.A., Edward C. Frackelton, B.A., Joseph T. Glessner, M.Sc., Cuiping Hou, M.Sc., F. George Otieno, M.Sc., Erin Santa, B.A., Kelly Thomas, B.A., Ryan M. Smith, B.A., Wendy R. Glaberson, B.A., Maria Garris, B.A., Rosetta M. Chiavacci, B.S.N., Terri H. Beaty, Ph.D., Ingo Ruczinski, Ph.D., Jordan M. Orange, M.D., Ph.D., Julian Allen, M.D., Jonathan M. Spergel, M.D., Ph.D., Robert Grundmeier, M.D., Ph.D., Rasika A. Mathias, Sc.D., Jason D. Christie, M.D., Erika von Mutius, M.D., William O.C. Cookson, M.D., Michael Kabesch, M.D., Miriam F. Moffatt, Ph.D., Michael M. Grunstein, M.D., Ph.D., Kathleen C. Barnes, Ph.D., Marcella Devoto, Ph.D., Mark Magnusson, M.D., Hongzhe Li, Ph.D., Struan F.A. Grant, Ph.D., Hans Bisgaard, M.D., and Hakon Hakonarson, M.D., Ph.D.

N Engl J Med 2010; 362:36-44 | [January 7, 2010](#)

Online phenotype association resources

- NHGRI's Catalog of Published GWAS:

<http://www.genome.gov/26525384>

- SNPedia:

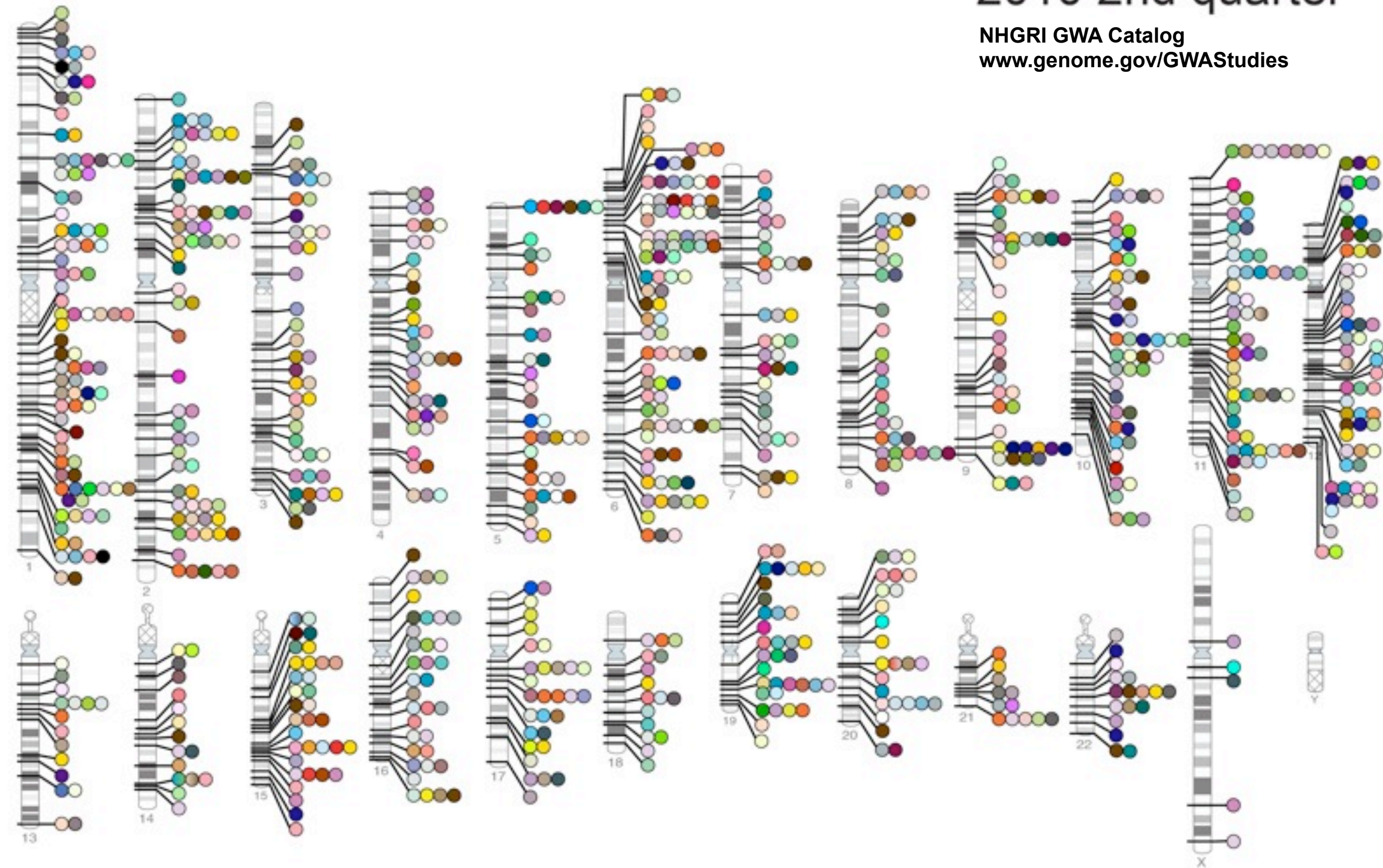
<http://www.snpedia.com>

**Published Genome-Wide Associations through 6/2010,
904 published GWA at $p \leq 5 \times 10^{-8}$ for 165 traits**

2010 2nd quarter


NHGRI GWA Catalog

www.genome.gov/GWAStudies



Acute lymphoblastic leukemia	Cleft lip/palate	Homocysteine levels	Osteoporosis	Serum metabolites
Adhesion molecules	Cognitive function	Idiopathic pulmonary fibrosis	Otosclerosis	Skin pigmentation
Adiponectin levels	Conduct disorder	IgE levels	Other metabolic traits	Smoking behavior
Age-related macular degeneration	Colorectal cancer	Inflammatory bowel disease	Ovarian cancer	Speech perception
AIDS progression	Corneal thickness	Intracranial aneurysm	Pancreatic cancer	Sphingolipid levels
Alcohol dependence	Coronary disease	Iris color	Pain	Statin-induced myopathy
Alzheimer disease	Creutzfeldt-Jakob disease	Iron status markers	Paget's disease	Stroke
Amyotrophic lateral sclerosis	Crohn's disease	Ischemic stroke	Panic disorder	Systemic lupus erythematosus
Angiotensin-converting enzyme activity	Cutaneous nevi	Juvenile idiopathic arthritis	Parkinson's disease	Systemic sclerosis
Ankylosing spondylitis	Dermatitis	Kidney stones	Periodontitis	Telomere length
Arterial stiffness	Drug-induced liver injury	LDL cholesterol	Peripheral arterial disease	Testicular germ cell tumor
Atherosclerosis in HIV	Eosinophil count	Leprosy	Phosphatidylcholine levels	Thyroid cancer
Atrial fibrillation	Eosinophilic esophagitis	Leptin receptor levels	Phytosterol levels	Tooth development
Attention deficit hyperactivity disorder	Erythrocyte parameters	Liver enzymes	Platelet count	Total cholesterol
Autism	Esophageal cancer	LP (a) levels	Primary biliary cirrhosis	Triglycerides
Basal cell cancer	Essential tremor	LpPLA(2) activity and mass	PR interval	Type 1 diabetes
Bipolar disorder	Exfoliation glaucoma	Lung cancer	Prostate cancer	Type 2 diabetes
Biliary atresia	Eye color traits	Major mood disorders	Protein levels	Ulcerative colitis
Bilirubin	F cell distribution	Malaria	Psoriasis	Urate
Birth weight	Fibrinogen levels	Male pattern baldness	Pulmonary funct. COPD	Venous thromboembolism
Bladder cancer	Folate pathway vitamins	Matrix metalloproteinase levels	QRS interval	Vertical cup-disc ratio
Blond or brown hair	Freckles and burning	MCP-1	QT interval	Vitamin B12 levels
Blood pressure	Gallstones	Melanoma	Quantitative traits	Vitamin D insufficiency
Blue or green eyes	Glioma	Menarche & menopause	Recombination rate	Vitiligo
BMI, waist circumference	Glycemic traits	Multiple sclerosis	Red vs.non-red hair	Warfarin dose
Bone density	Hair color	Myeloproliferative neoplasms	Renal function	Weight
Breast cancer	Hair morphology	Narcolepsy	Response to antidepressants	White cell count
C-reactive protein	HDL cholesterol	Nasopharyngeal cancer	Response to antipsychotic therapy	YKL-40 levels
Cardiac structure/function	Heart failure	Neuroblastoma	Response to hepatitis C treat	
Carnitine levels	Heart rate	Nicotine dependence	Response to statin therapy	
Carotenoid/tocopherol levels	Height	Obesity	Restless legs syndrome	
Celiac disease	Hemostasis parameters	Open angle glaucoma	Rheumatoid arthritis	
Chronic lymphocytic leukemia	Hepatitis	Open personality	Schizophrenia	
	Hirschsprung's disease	Optic disc parameters		
	HIV-1 control	Osteoarthritis		

Earwax

[rs17822931](#) determines wet vs dry earwax [[PMID 16444273](#) 

This can also be used to distinguish asian ancestry.

NCBI [coffeebreak](#)  introduction

Category: [Is a medical condition](#)

[The DNA Ancestry Project](#) Discover Your Ancestry with DNA. Find Ethnic and Geographic Origins. www.DNAAncestry

[High throughput screening](#) Unknown mutations Detection BRCA1 & BRCA2 www.fluigent.com/

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From genotype to phenotype

- 99.9% of human DNA is identical to another person
- 0.1% → over 80% are single nucleotide polymorphisms (SNPs)
- The genotype of an organism is the inherited instructions within the DNA
- A phenotype is any observable characteristic or trait of an organism

Exercise: Genotype to Phenotype

<http://wiki.cbs.dtu.dk/teachingmaterials/index.php/ExGenotype2PhenotypeLite>